

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/540,546
Source: Ifwo
Date Processed by STIC: 11/27/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/27/2006

PATENT APPLICATION: US/10/540,546

TIME: 14:23:18

Input Set : A:\274130.Substitute.Sequence_Listing.TXT

Output Set: N:\CRF4\11272006\J540546.raw

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3 <110> APPLICANT: Fujisawa Pharmaceutical Co., Ltd.
4     Matsuoka, Hideaki
5     Fujimura, Takao
6     Hayashi, Masako
7     Aramori, Ichiro
9 <120> TITLE OF INVENTION: New methods for selecting an immunosuppressive agent
11 <130> FILE REFERENCE: 274130USOPCT
W--> 12 <140> CURRENT APPLICATION NUMBER: 10/540,546
13 <141> CURRENT FILING DATE: 2005-06-24
15 <150> PRIOR APPLICATION NUMBER: JP2002-378800
16 <151> PRIOR FILING DATE: 2002-12-27
18 <160> NUMBER OF SEQ ID NOS: 86
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3255
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(3255)
30 <223> OTHER INFORMATION: human histone deacetylase-4 (HDAC4) gene
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33 atg agc tcc caa agc cat cca gat gga ctt tct ggc cga gac cag cca      48
34 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
35 1          5          10          15
37 gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg      96
38 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
39          20          25          30
41 gat gtg gcc acg gcg ctg cct ctg caa gtg gcc ccc tcg gca gtg ccc      144
42 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
43          35          40          45
45 atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg      192
46 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
47          50          55          60
49 gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag      240
50 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
51 65          70          75          80
53 aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag      288
54 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
55          85          90          95
57 cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc      336
58 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
59          100          105          110

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61 aag caa caa cag gag atg ctg gcc atg aag cac cag cag gag ctg ctg      384
62 Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
63      115      120      125
65 gaa cac cag cgg aag ctg gag agg cac cgc cag gag cag gag ctg gag      432
66 Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
67      130      135      140
69 aag cag cac cgg cag cag aag ctg cag cag ctc aag aac aag gag aag      480
70 Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
71      145      150      155      160
73 ggc aaa gag agt gcc gtg gcc agc aca gaa gtg aag atg aag tta caa      528
74 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
75      165      170      175
77 gaa ttt gtc ctc aat aaa aag aag gcg ctg gcc cac cgg aat ctg aac      576
78 Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
79      180      185      190
81 cac tgc att tcc agc gac cct cgc tac tgg tac ggg aaa acg cag cac      624
82 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
83      195      200      205
85 agt tcc ctt gac cag agt tct cca ccc cag agc gga gtg tgc acc tcc      672
86 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
87      210      215      220
89 tat aac cac ccg gtc ctg gga atg tac gac gcc aaa gat gac ttc cct      720
90 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
91      225      230      235      240
93 ctt agg aaa aca gct tct gaa ccg aat ctg aaa tta cgg tcc agg cta      768
94 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
95      245      250      255
97 aag cag aaa gtg gcc gaa aga cgg agc agc ccc ctg tta cgc agg aaa      816
98 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
99      260      265      270
101 gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca      864
102 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
103      275      280      285
105 gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac      912
106 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
107      290      295      300
109 aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc      960
110 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
111      305      310      315      320
113 ccc agc atc ccg gcg gag acg agt ttg gcg cac aga ctt gtg gca cga      1008
114 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
115      325      330      335
117 gaa ggc tgc gcc gct cca ctt ccc ctc tac aca tgc cca tcc ttg ccc      1056
118 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
119      340      345      350
121 aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg      1104
122 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
123      355      360      365
125 ggc cag cag gac acc gag aga ctc acc ctt ccc gcc ctc cag cag agg      1152

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126	Gly	Gln	Gln	Asp	Thr	Glu	Arg	Leu	Thr	Leu	Pro	Ala	Leu	Gln	Gln	Arg	
127		370					375					380					
129	ctc	tcc	ctt	ttc	ccc	ggc	acc	cac	ctc	act	ccc	tac	ctg	agc	acc	tcg	1200
130	Leu	Ser	Leu	Phe	Pro	Gly	Thr	His	Leu	Thr	Pro	Tyr	Leu	Ser	Thr	Ser	
131	385					390					395				400		
133	ccc	ttg	gag	cgg	gac	gga	ggg	gca	gcg	cac	agc	cct	ctt	ctg	cag	cac	1248
134	Pro	Leu	Glu	Arg	Asp	Gly	Gly	Ala	Ala	His	Ser	Pro	Leu	Leu	Gln	His	
135				405						410					415		
137	atg	gtc	tta	ctg	gag	cag	cca	ccg	gca	caa	gca	ccc	ctc	gtc	aca	ggc	1296
138	Met	Val	Leu	Leu	Glu	Gln	Pro	Pro	Ala	Gln	Ala	Pro	Leu	Val	Thr	Gly	
139				420					425					430			
141	ctg	gga	gca	ctg	ccc	ctc	cac	gca	cag	tcc	ttg	gtt	ggt	gca	gac	cgg	1344
142	Leu	Gly	Ala	Leu	Pro	Leu	His	Ala	Gln	Ser	Leu	Val	Gly	Ala	Asp	Arg	
143			435					440						445			
145	gtg	tcc	ccc	tcc	atc	cac	aag	ctg	cgg	cag	cac	cgc	cca	ctg	ggg	cgg	1392
146	Val	Ser	Pro	Ser	Ile	His	Lys	Leu	Arg	Gln	His	Arg	Pro	Leu	Gly	Arg	
147		450					455					460					
149	acc	cag	tcg	gcc	ccg	ctg	ccc	cag	aac	gcc	cag	gct	ctg	cag	cac	ctg	1440
150	Thr	Gln	Ser	Ala	Pro	Leu	Pro	Gln	Asn	Ala	Gln	Ala	Leu	Gln	His	Leu	
151	465				470					475					480		
153	gtc	atc	cag	cag	cag	cat	cag	cag	ttt	ctg	gag	aaa	cac	aag	cag	cag	1488
154	Val	Ile	Gln	Gln	Gln	His	Gln	Gln	Phe	Leu	Glu	Lys	His	Lys	Gln	Gln	
155				485					490					495			
157	ttc	cag	cag	cag	caa	ctg	cag	atg	aac	aag	atc	atc	ccc	aag	cca	agc	1536
158	Phe	Gln	Gln	Gln	Gln	Leu	Gln	Met	Asn	Lys	Ile	Ile	Pro	Lys	Pro	Ser	
159				500					505					510			
161	gag	cca	gcc	cgg	cag	ccg	gag	agc	cac	ccg	gag	gag	acg	gag	gag	gag	1584
162	Glu	Pro	Ala	Arg	Gln	Pro	Glu	Ser	His	Pro	Glu	Glu	Thr	Glu	Glu	Glu	
163			515					520					525				
165	ctc	cgt	gag	cac	cag	gct	ctg	ctg	gac	gag	ccc	tac	ctg	gac	cgg	ctg	1632
166	Leu	Arg	Glu	His	Gln	Ala	Leu	Leu	Asp	Glu	Pro	Tyr	Leu	Asp	Arg	Leu	
167		530					535					540					
169	ccg	ggg	cag	aag	gag	gcg	cac	gca	cag	gcc	ggc	gtg	cag	gtg	aag	cag	1680
170	Pro	Gly	Gln	Lys	Glu	Ala	His	Ala	Gln	Ala	Gly	Val	Gln	Val	Lys	Gln	
171	545				550					555					560		
173	gag	ccc	att	gag	agc	gat	gag	gaa	gag	gca	gag	ccc	cca	cgg	gag	gtg	1728
174	Glu	Pro	Ile	Glu	Ser	Asp	Glu	Glu	Glu	Ala	Glu	Pro	Pro	Arg	Glu	Val	
175				565					570					575			
177	gag	ccg	ggc	cag	cgc	cag	ccc	agt	gag	cag	gag	ctg	ctc	ttc	aga	cag	1776
178	Glu	Pro	Gly	Gln	Arg	Gln	Pro	Ser	Glu	Gln	Glu	Leu	Leu	Phe	Arg	Gln	
179				580					585					590			
181	caa	gcc	ctc	ctg	ctg	gag	cag	cag	cgg	atc	cac	cag	ctg	agg	aac	tac	1824
182	Gln	Ala	Leu	Leu	Leu	Glu	Gln	Gln	Arg	Ile	His	Gln	Leu	Arg	Asn	Tyr	
183			595					600					605				
185	cag	gcg	tcc	atg	gag	gcc	gcc	ggc	atc	ccc	gtg	tcc	ttc	ggc	ggc	cac	1872
186	Gln	Ala	Ser	Met	Glu	Ala	Ala	Gly	Ile	Pro	Val	Ser	Phe	Gly	Gly	His	
187		610					615					620					
189	agg	cct	ctg	tcc	cgg	gcg	cag	tcc	tca	ccc	gcg	tct	gcc	acc	ttc	ccc	1920
190	Arg	Pro	Leu	Ser	Arg	Ala	Gln	Ser	Ser	Pro	Ala	Ser	Ala	Thr	Phe	Pro	

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257 ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga      2736
258 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
259          900          905          910
261 acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg      2784
262 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
263          915          920          925
265 gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccg acc cct ctt ggg      2832
266 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
267          930          935          940
269 ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg      2880
270 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
271 945          950          955          960
273 atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac      2928
274 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
275          965          970          975
277 gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg      2976
278 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
279          980          985          990
281 ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga      3024
282 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
283          995          1000          1005
285 ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac      3072
286 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
287          1010          1015          1020
289 agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt      3120
290 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
291 1025          1030          1035          1040
293 tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc      3168
294 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
295          1045          1050          1055
297 acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga      3216
298 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
299          1060          1065          1070
301 cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag      3255
302 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
303          1075          1080
306 <210> SEQ ID NO: 2
307 <211> LENGTH: 1084
308 <212> TYPE: PRT
309 <213> ORGANISM: Homo sapiens
311 <400> SEQUENCE: 2
312 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
313 1          5          10          15
315 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
316          20          25          30
318 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
319          35          40          45
321 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
322          50          55          60

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; N Pos. 4,5,6,7,8,9,12,56

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:60; Line(s) 4155
Seq#:61; Line(s) 4168
Seq#:62; Line(s) 4181
Seq#:63; Line(s) 4194
Seq#:66; Line(s) 4233
Seq#:67; Line(s) 4246
Seq#:68; Line(s) 4259
Seq#:69; Line(s) 4272
Seq#:74; Line(s) 4337
Seq#:75; Line(s) 4350
Seq#:76; Line(s) 4363
Seq#:77; Line(s) 4376

VERIFICATION SUMMARY

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L:12 M:283 W: Missing Blank Line separator, <140> field identifier

L:3600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0